

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: OLSEN, HENRIK S.
RUBEN, STEVEN
NI, JIAN
MURPHY, MARIANNE
GENTZ, REINER
- (ii) TITLE OF INVENTION: FC RECEPTORS AND POLYPEPTIDES
- (iii) NUMBER OF SEQUENCES: 32
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: HUMAN GENOME SCIENCES, INC.
 - (B) STREET: 9410 KEY WEST AVENUE
 - (C) CITY: ROCKVILLE
 - (D) STATE: MD
 - (E) COUNTRY: US
 - (F) ZIP: 20850
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: BROOKES, ALLAN A.
 - (B) REGISTRATION NUMBER: 36,373
 - (C) REFERENCE/DOCKET NUMBER: PF363
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (301) 309-8504
 - (B) TELEFAX: (301) 309-8512

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1552 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 82..1362

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 82..142

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 145..1362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCAGGAATTC GGCACGAGCC TCTGTCCTGC CAGCACCGAG GGCTCATCCA TCCACAGAGC	60
AGTGCAGTGG GAGGAGACGC C ATG ACC CCC ATC CTC ACG GTC CTG ATC TGT	111
Met Thr Pro Ile Leu Thr Val Leu Ile Cys	
-21 -20 -15	
CTC GGG CCC CTC CCC AAG CCC ACC CTC TGG GCT GAG CCA GGC TCT GTG	159
Leu Gly Pro Leu Pro Lys Pro Thr Leu Trp Ala Glu Pro Gly Ser Val	
-10 -5 1 5	
ATC ACC CAA GGG AGT CCT GTG ACC CTC AGG TGT CAG GGG AGC CTG GAG	207
Ile Thr Gln Gly Ser Pro Val Thr Leu Arg Cys Gln Gly Ser Leu Glu	
10 15 20	
ACG CAG GAG TAC CAT CTA TAT AGA GAA AAG AAA ACA GCA CTC TGG ATT	255
Thr Gln Glu Tyr His Leu Tyr Arg Glu Lys Lys Thr Ala Leu Trp Ile	
25 30 35	
ACA CGG ATC CCA CAG GAG CTT GTG AAG AAG GGC CAG TTC CCC ATC CTA	303
Thr Arg Ile Pro Gln Glu Leu Val Lys Lys Gly Gln Phe Pro Ile Leu	
40 45 50	
TCC ATC ACC TGG GAA CAT GCA GGG CGG TAT TGC TGT ATC TAT GGC AGC	351
Ser Ile Thr Trp Glu His Ala Gly Arg Tyr Cys Cys Ile Tyr Gly Ser	
55 60 65	
CAC ACT GCA GGC CTC TCA GAG AGC AGT GAC CCC CTG GAG CTG GTG GTG	399
His Thr Ala Gly Leu Ser Glu Ser Ser Asp Pro Leu Glu Leu Val Val	
70 75 80 85	
ACA GGA GCC TAC AGC AAA CCC ACC CTC TCA GCT CTG CCC AGC CCT GTG	447
Thr Gly Ala Tyr Ser Lys Pro Thr Leu Ser Ala Leu Pro Ser Pro Val	
90 95 100	
GTG ACC TCA GGA GGG AAT GTG ACC ATC CAG TGT GAC TCA CAG GTG GCA	495
Val Thr Ser Gly Gly Asn Val Thr Ile Gln Cys Asp Ser Gln Val Ala	
105 110 115	
TTT GAT GGC TTC ATT CTG TGT AAG GAA GGA GAA GAT GAA CAC CCA CAA	543
Phe Asp Gly Phe Ile Leu Cys Lys Glu Gly Glu Asp Glu His Pro Gln	
120 125 130	
TGC CTG AAC TCC CAT TCC CAT GCC CGT GGG TCA TCC CGG GCC ATC TTC	591
Cys Leu Asn Ser His Ser His Ala Arg Gly Ser Ser Arg Ala Ile Phe	
135 140 145	
TCC GTG GGC CCC GTG AGC CCA AGT CGC AGG TGG TCG TAC AGG TGC TAT	639
Ser Val Gly Pro Val Ser Pro Ser Arg Arg Trp Ser Tyr Arg Cys Tyr	
150 155 160 165	
GGT TAT GAC TCG CGC GCT CCC TAT GTG TGG TCT CTA CCC AGT GAT CTC	687
Gly Tyr Asp Ser Arg Ala Pro Tyr Val Trp Ser Leu Pro Ser Asp Leu	

170	175	180	
CTG GGG CTC CTG GTC CCA GGT GTT TCT AAG AAG CCA TCA CTC TCA GTG Leu Gly Leu Leu Val Pro Gly Val Ser Lys Lys Pro Ser Leu Ser Val			735
185	190	195	
CAG CCG GGT CCT GTC GTG GCC CCT GGG GAG AAG CTG ACC TTC CAG TGT Gln Pro Gly Pro Val Val Ala Pro Gly Glu Lys Leu Thr Phe Gln Cys			783
200	205	210	
GGC TCT GAT GCC GGC TAC GAC AGA TTT GTT CTG TAC AAG GAG TGG GGA Gly Ser Asp Ala Gly Tyr Asp Arg Phe Val Leu Tyr Lys Glu Trp Gly			831
215	220	225	
CGT GAC TTC CTC CAG CGC CCT GGC CGG CAG CCC CAG GCT GGG CTC TCC Arg Asp Phe Leu Gln Arg Pro Gly Arg Gln Pro Gln Ala Gly Leu Ser			879
230	235	240	245
CAG GCC AAC TTC ACC CTG GGC CCT GTG AGC CGC TCC TAC GGG GGC CAG Gln Ala Asn Phe Thr Leu Gly Pro Val Ser Arg Ser Tyr Gly Gly Gln			927
250	255	260	
TAC ACA TGC TCC GGT GCA TAC AAC CTC TCC TCC GAG TGG TCG GCC CCC Tyr Thr Cys Ser Gly Ala Tyr Asn Leu Ser Ser Glu Trp Ser Ala Pro			975
265	270	275	
AGC GAC CCC CTG GAC ATC CTG ATC ACA GGA CAG ATC CGT GCC AGA CCC Ser Asp Pro Leu Asp Ile Leu Ile Thr Gly Gln Ile Arg Ala Arg Pro			1023
280	285	290	
TTC CTC TCC GTG CGG CCG GGC CCC ACA GTG GCC TCA GGA GAG AAC GTG Phe Leu Ser Val Arg Pro Gly Pro Thr Val Ala Ser Gly Glu Asn Val			1071
295	300	305	
ACC CTG CTG TGT CAG TCA CAG GGA GGG ATG CAC ACT TTC CTT TTG ACC Thr Leu Leu Cys Gln Ser Gln Gly Gly Met His Thr Phe Leu Leu Thr			1119
310	315	320	325
AAG GAG GGG GCA GCT GAT TCC CCG CTG CGT CTA AAA TCA AAG CGC CAA Lys Glu Gly Ala Ala Asp Ser Pro Leu Arg Leu Lys Ser Lys Arg Gln			1167
330	335	340	
TCT CAT AAG TAC CAG GCT GAA TTC CCC ATG AGT CCT GTG ACC TCG GCC Ser His Lys Tyr Gln Ala Glu Phe Pro Met Ser Pro Val Thr Ser Ala			1215
345	350	355	
CAC GCG GGG ACC TAC AGG TGC TAC GGC TCA CTC AGC TCC AAC CCC TAC His Ala Gly Thr Tyr Arg Cys Tyr Gly Ser Leu Ser Ser Asn Pro Tyr			1263
360	365	370	
CTG CTG ACT CAC CCC AGT GAC CCC CTG GAG CTC GTG GTC TCA GGA GCA Leu Leu Thr His Pro Ser Asp Pro Leu Glu Leu Val Val Ser Gly Ala			1311
375	380	385	
GCT GAG ACC CTC AGC CCA CCA CAA AAC AAG TCC GAC TCC AAG GCT GGT Ala Glu Thr Leu Ser Pro Pro Gln Asn Lys Ser Asp Ser Lys Ala Gly			1359
390	395	400	405
GAG TGAGGAGATG CTTGCCGTGA TGACGCTGGG CACAGAGGGT CAGGTCCTGT Glu			1412
CAAGAGGAGC TGGGTGTCCT GGGTGGACAT TTGAAGAATT ATATTCATTC CAACTTGAAG			1472

AATTATTCAA CACCTTTAAC AATGTATATG TGAAGTACTT TATTCTTTCA TATTTTAAAA 1532

ATAAAAGATA ATTATCCATG 1552

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Thr	Pro	Ile	Leu	Thr	Val	Leu	Ile	Cys	Leu	Gly	Pro	Leu	Pro	Lys	
-21	-20					-15					-10					
Pro	Thr	Leu	Trp	Ala	Glu	Pro	Gly	Ser	Val	Ile	Thr	Gln	Gly	Ser	Pro	
-5					1				5					10		
Val	Thr	Leu	Arg	Cys	Gln	Gly	Ser	Leu	Glu	Thr	Gln	Glu	Tyr	His	Leu	
			15					20					25			
Tyr	Arg	Glu	Lys	Lys	Thr	Ala	Leu	Trp	Ile	Thr	Arg	Ile	Pro	Gln	Glu	
		30					35					40				
Leu	Val	Lys	Lys	Gly	Gln	Phe	Pro	Ile	Leu	Ser	Ile	Thr	Trp	Glu	His	
	45					50					55					
Ala	Gly	Arg	Tyr	Cys	Cys	Ile	Tyr	Gly	Ser	His	Thr	Ala	Gly	Leu	Ser	
60				65						70					75	
Glu	Ser	Ser	Asp	Pro	Leu	Glu	Leu	Val	Val	Thr	Gly	Ala	Tyr	Ser	Lys	
				80					85					90		
Pro	Thr	Leu	Ser	Ala	Leu	Pro	Ser	Pro	Val	Val	Thr	Ser	Gly	Gly	Asn	
			95					100					105			
Val	Thr	Ile	Gln	Cys	Asp	Ser	Gln	Val	Ala	Phe	Asp	Gly	Phe	Ile	Leu	
		110					115					120				
Cys	Lys	Glu	Gly	Glu	Asp	Glu	His	Pro	Gln	Cys	Leu	Asn	Ser	His	Ser	
	125					130					135					
His	Ala	Arg	Gly	Ser	Ser	Arg	Ala	Ile	Phe	Ser	Val	Gly	Pro	Val	Ser	
140					145					150					155	
Pro	Ser	Arg	Arg	Trp	Ser	Tyr	Arg	Cys	Tyr	Gly	Tyr	Asp	Ser	Arg	Ala	
			160						165					170		
Pro	Tyr	Val	Trp	Ser	Leu	Pro	Ser	Asp	Leu	Leu	Gly	Leu	Leu	Val	Pro	
			175					180					185			
Gly	Val	Ser	Lys	Lys	Pro	Ser	Leu	Ser	Val	Gln	Pro	Gly	Pro	Val	Val	
		190					195					200				
Ala	Pro	Gly	Glu	Lys	Leu	Thr	Phe	Gln	Cys	Gly	Ser	Asp	Ala	Gly	Tyr	
	205					210					215					
Asp	Arg	Phe	Val	Leu	Tyr	Lys	Glu	Trp	Gly	Arg	Asp	Phe	Leu	Gln	Arg	

220		225		230		235
Pro Gly Arg Gln	Pro Gln Ala Gly Leu Ser Gln Ala Asn Phe Thr Leu					
	240		245		250	
Gly Pro Val Ser Arg Ser Tyr Gly Gly Gln Tyr Thr Cys Ser Gly Ala						
	255		260		265	
Tyr Asn Leu Ser Ser Glu Trp Ser Ala Pro Ser Asp Pro Leu Asp Ile						
	270		275		280	
Leu Ile Thr Gly Gln Ile Arg Ala Arg Pro Phe Leu Ser Val Arg Pro						
	285		290		295	
Gly Pro Thr Val Ala Ser Gly Glu Asn Val Thr Leu Leu Cys Gln Ser						
	300		305		310	315
Gln Gly Gly Met His Thr Phe Leu Leu Thr Lys Glu Gly Ala Ala Asp						
	320		325		330	
Ser Pro Leu Arg Leu Lys Ser Lys Arg Gln Ser His Lys Tyr Gln Ala						
	335		340		345	
Glu Phe Pro Met Ser Pro Val Thr Ser Ala His Ala Gly Thr Tyr Arg						
	350		355		360	
Cys Tyr Gly Ser Leu Ser Ser Asn Pro Tyr Leu Leu Thr His Pro Ser						
	365		370		375	
Asp Pro Leu Glu Leu Val Val Ser Gly Ala Ala Glu Thr Leu Ser Pro						
	380		385		390	395
Pro Gln Asn Lys Ser Asp Ser Lys Ala Gly Glu						
	400		405			

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1410 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
- (A) NAME/KEY: CDS
 - (B) LOCATION: 37..826

- (ix) FEATURE:
- (A) NAME/KEY: sig_peptide
 - (B) LOCATION: 37..88

- (ix) FEATURE:
- (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 91..826

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ACCCACGCGT CCGCACTCTA GCGGTATCTG CCCACC ATG GCC CTG GTG CTG ATC
Met Ala Leu Val Leu Ile

															-18	-15
CTC	CAG	CTG	CTG	ACC	CTC	TGG	CCT	CTG	TGT	CAC	ACA	GAC	ATC	ACT	CCG	102
Leu	Gln	Leu	Leu	Thr	Leu	Trp	Pro	Leu	Cys	His	Thr	Asp	Ile	Thr	Pro	
-10					-5					1						
TCT	GTC	CCC	CCA	GCT	TCA	TAC	CAC	CCT	AAG	CCA	TGG	CTG	GGA	GCT	CAG	150
Ser	Val	Pro	Pro	Ala	Ser	Tyr	His	Pro	Lys	Pro	Trp	Leu	Gly	Ala	Gln	
5					10					15					20	
CCG	GCT	ACA	GTT	GTG	ACC	CCT	GGG	GTC	AAC	GTG	ACC	TTG	AGA	TGC	CGG	198
Pro	Ala	Thr	Val	Val	Thr	Pro	Gly	Val	Asn	Val	Thr	Leu	Arg	Cys	Arg	
25					30					35						
GCA	CCC	CAA	CCC	GCT	TGG	AGA	TTT	GGA	CTT	TTC	AAG	CCT	GGA	GAG	ATC	246
Ala	Pro	Gln	Pro	Ala	Trp	Arg	Phe	Gly	Leu	Phe	Lys	Pro	Gly	Glu	Ile	
40					45					50						
GCT	CCC	CTT	CTC	TTC	CGG	GAT	GTG	TCC	TCC	GAG	CTG	GCA	GAA	TTC	TTT	294
Ala	Pro	Leu	Leu	Phe	Arg	Asp	Val	Ser	Ser	Glu	Leu	Ala	Glu	Phe	Phe	
55					60					65						
CTG	GAG	GAG	GTG	ACT	CCA	GCC	CAA	GGG	GGA	AGT	TAC	CGC	TGC	TGC	TAC	342
Leu	Glu	Glu	Val	Thr	Pro	Ala	Gln	Gly	Gly	Ser	Tyr	Arg	Cys	Cys	Tyr	
70					75					80						
CGA	AGG	CCA	GAC	TGG	GGG	CCG	GGT	GTC	TGG	TCC	CAG	CCC	AGC	GAT	GTC	390
Arg	Arg	Pro	Asp	Trp	Gly	Pro	Gly	Val	Trp	Ser	Gln	Pro	Ser	Asp	Val	
85					90					95					100	
CTG	GAG	CTG	CTG	GTG	ACA	GAG	GAG	CTG	CCG	CGG	CCG	TCG	CTG	GTG	GCG	438
Leu	Glu	Leu	Leu	Val	Thr	Glu	Glu	Leu	Pro	Arg	Pro	Ser	Leu	Val	Ala	
105					110					115						
CTG	CCC	GGG	CCG	GTG	GTG	GGT	CCT	GGC	GCC	AAC	GTG	AGC	CTG	CGC	TGC	486
Leu	Pro	Gly	Pro	Val	Val	Gly	Pro	Gly	Ala	Asn	Val	Ser	Leu	Arg	Cys	
120					125					130						
GCG	GGC	CGC	CTG	CGG	AAC	ATG	AGC	TTC	GTG	CTG	TAC	CGC	GAG	GGC	GTG	534
Ala	Gly	Arg	Leu	Arg	Asn	Met	Ser	Phe	Val	Leu	Tyr	Arg	Glu	Gly	Val	
135					140					145						
GCG	GCC	CCG	CTG	CAG	TAC	CGC	CAC	TCC	GCG	CAG	CCC	TGG	GCC	GAC	TTC	582
Ala	Ala	Pro	Leu	Gln	Tyr	Arg	His	Ser	Ala	Gln	Pro	Trp	Ala	Asp	Phe	
150					155					160						
ACG	CTG	CTG	GGC	GCC	CGC	GCC	CCC	GGC	ACC	TAC	AGC	TGC	TAC	TAT	CAC	630
Thr	Leu	Leu	Gly	Ala	Arg	Ala	Pro	Gly	Thr	Tyr	Ser	Cys	Tyr	Tyr	His	
165					170					175					180	
ACG	CCC	TCC	GCG	CCC	TAC	GTG	CTG	TCG	CAG	CGC	AGC	GAG	GTG	CTG	GTC	678
Thr	Pro	Ser	Ala	Pro	Tyr	Val	Leu	Ser	Gln	Arg	Ser	Glu	Val	Leu	Val	
185					190					195						
ATC	AGC	TGG	GAA	GAC	TCT	GGC	TCC	TCC	GAC	TAC	ACC	CGG	GGG	AAC	CTA	726
Ile	Ser	Trp	Glu	Asp	Ser	Gly	Ser	Ser	Asp	Tyr	Thr	Arg	Gly	Asn	Leu	
200					205					210						
GTC	CGC	CTG	GGG	CTG	GCC	GGG	CTG	GTC	CTC	ATC	TCC	CTG	GGC	GCG	CTG	774
Val	Arg	Leu	Gly	Leu	Ala	Gly	Leu	Val	Leu	Ile	Ser	Leu	Gly	Ala	Leu	
215					220					225						
GTC	ACT	TTT	GAC	TGG	CGC	AGT	CAG	AAC	CGC	GCT	CCT	GCT	GGT	ATC	CGC	822

Val Thr Phe Asp Trp Arg Ser Gln Asn Arg Ala Pro Ala Gly Ile Arg
 230 235 240

CCC T GAGCCCCAGG AGCACTGCAG CCGGAGACTT CCAACCTGAG TGGCGGAGAA 876
 Pro
 245

GCTGGGACCC TGGGCTGGAC TGTCCTTTCC TGCAGCCCCA CAGTCCTGCT GGCTGAGCTC 936
 CGCGGAACGG TCCTTAGACC CCGCTGTGCC CTGTGCTGTA GCTTCTTTCC AGGCCTTTCC 996
 CAAGGAGTAG CTGAAAGGAA GACGCGATTA GTGGTTAAGA CTTCCAAGCC AGAAGACAGA 1056
 GGGTTCGAAT CCCAGCACTG CCGTCTACTC ACTGTAGTAG TAGCAGCTAC AGAAAGGTAG 1116
 TAGTGAGACG TGAAGCCAGC TGGACTTCCT GGGTTGAATG GGGACCTGGA GAACTTTTCT 1176
 GTCTTACAAG AGGATTGTAA AATGGACCAA TCAGCACTCT GTAAGATGGA CCAATCAGCG 1236
 CTCTGTAAAA TGGACCAATC AGCAGGACAT GGGCGGGGAC AATAAGGGAA TAAAAGCTGG 1296
 CGAGCGCGGC ACCCCACCAG AGTCTGCTTC CACGCTGTGG GAGCTTTGTT CTCCTGCTCT 1356
 ACACAATAAA TCTTGCTGCT GCTAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAA 1410

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Leu Val Leu Ile Leu Gln Leu Leu Thr Leu Trp Pro Leu Cys
 -18 -15 -10 -5

His Thr Asp Ile Thr Pro Ser Val Pro Pro Ala Ser Tyr His Pro Lys
 1 5 10

Pro Trp Leu Gly Ala Gln Pro Ala Thr Val Val Thr Pro Gly Val Asn
 15 20 25 30

Val Thr Leu Arg Cys Arg Ala Pro Gln Pro Ala Trp Arg Phe Gly Leu
 35 40 45

Phe Lys Pro Gly Glu Ile Ala Pro Leu Leu Phe Arg Asp Val Ser Ser
 50 55 60

Glu Leu Ala Glu Phe Phe Leu Glu Glu Val Thr Pro Ala Gln Gly Gly
 65 70 75

Ser Tyr Arg Cys Cys Tyr Arg Arg Pro Asp Trp Gly Pro Gly Val Trp
 80 85 90

Ser Gln Pro Ser Asp Val Leu Glu Leu Leu Val Thr Glu Glu Leu Pro
 95 100 105 110

Arg Pro Ser Leu Val Ala Leu Pro Gly Pro Val Val Gly Pro Gly Ala
 115 120 125

Asn Val Ser Leu Arg Cys Ala Gly Arg Leu Arg Asn Met Ser Phe Val
 130 135 140
 Leu Tyr Arg Glu Gly Val Ala Ala Pro Leu Gln Tyr Arg His Ser Ala
 145 150 155
 Gln Pro Trp Ala Asp Phe Thr Leu Leu Gly Ala Arg Ala Pro Gly Thr
 160 165 170
 Tyr Ser Cys Tyr Tyr His Thr Pro Ser Ala Pro Tyr Val Leu Ser Gln
 175 180 185 190
 Arg Ser Glu Val Leu Val Ile Ser Trp Glu Asp Ser Gly Ser Ser Asp
 195 200 205
 Tyr Thr Arg Gly Asn Leu Val Arg Leu Gly Leu Ala Gly Leu Val Leu
 210 215 220
 Ile Ser Leu Gly Ala Leu Val Thr Phe Asp Trp Arg Ser Gln Asn Arg
 225 230 235
 Ala Pro Ala Gly Ile Arg Pro
 240 245

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1991 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 73..1942

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 73..118

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 121..1942

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCAGGAATTC GGCACGAGCA GCACTGAGGG CTCATCCCTC TGCAGAGCGC GGGGTCACCG 60
 GAAGGAGACG CC ATG ACG CCC GCC CTC ACA GCC CTG CTC TGC CTT GGG 108
 Met Thr Pro Ala Leu Thr Ala Leu Leu Cys Leu Gly
 -16 -15 -10 -5
 CTG AGT CTG GGC CCC AGG ACC CGC GTG CAG GCA GGG CCC TTC CCC AAA 156
 Leu Ser Leu Gly Pro Arg Thr Arg Val Gln Ala Gly Pro Phe Pro Lys
 1 5 10
 CCC ACC CTC TGG GCT GAG CCA GGC TCT GTG ATC AGC TGG GGG AGC CCC 204
 Pro Thr Leu Trp Ala Glu Pro Gly Ser Val Ile Ser Trp Gly Ser Pro

15	20	25	
GTG ACC ATC TGG TGT CAG GGG AGC CTG GAG GCC CAG GAG TAC CAA CTG Val Thr Ile Trp Cys Gln Gly Ser Leu Glu Ala Gln Glu Tyr Gln Leu 30 35 40			252
GAT AAA GAG GGA AGC CCA GAG CCC TTG GAC AGA AAT AAC CCA CTG GAA Asp Lys Glu Gly Ser Pro Glu Pro Leu Asp Arg Asn Asn Pro Leu Glu 45 50 55 60			300
CCC AAG AAC AAG GCC AGA TTC TCC ATC CCA TCC ATG ACA CAG CAC CAT Pro Lys Asn Lys Ala Arg Phe Ser Ile Pro Ser Met Thr Gln His His 65 70 75			348
GCA GGG AGA TAC CGC TGC CAC TAT TAC AGC TCT GCA GGC TGG TCA GAG Ala Gly Arg Tyr Arg Cys His Tyr Tyr Ser Ser Ala Gly Trp Ser Glu 80 85 90			396
CCC AGC GAC CCC CTG GAG CTG GTG ATG ACA GGA GCC TAT AGC AAA CCC Pro Ser Asp Pro Leu Glu Leu Val Met Thr Gly Ala Tyr Ser Lys Pro 95 100 105			444
ACC CTC TCA GCC CTG CCC AGC CCT GTG GTG GCC TCA GGG GGG AAT ATG Thr Leu Ser Ala Leu Pro Ser Pro Val Val Ala Ser Gly Gly Asn Met 110 115 120			492
ACC CTC CGA TGT GGC TCA CAG AAG AGA TAT CAC CAT TTT GTT CTG ATG Thr Leu Arg Cys Gly Ser Gln Lys Arg Tyr His His Phe Val Leu Met 125 130 135 140			540
AAG GAA GGA GAA CAC CAG CTC CCC CGG ACC CTG GAC TCA CAG CAG CTC Lys Glu Gly Glu His Gln Leu Pro Arg Thr Leu Asp Ser Gln Gln Leu 145 150 155			588
CAC AGT GGG GGG TTC CAG GCC CTG TTC CCT GTG GGC CCC GTG AAC CCC His Ser Gly Gly Phe Gln Ala Leu Phe Pro Val Gly Pro Val Asn Pro 160 165 170			636
AGC CAC AGG TGG AGG TTC ACA TGC TAT TAC TAT TAT ATG AAC ACC CCC Ser His Arg Trp Arg Phe Thr Cys Tyr Tyr Tyr Tyr Met Asn Thr Pro 175 180 185			684
CGG GTG TGG TCC CAC CCC AGT GAC CCC CTG GAG ATT CTG CCC TCA GGC Arg Val Trp Ser His Pro Ser Asp Pro Leu Glu Ile Leu Pro Ser Gly 190 195 200			732
GTG TCT AGG AAG CCC TCC CTC CTG ACC CTG CAG GGC CCT GTC CTG GCC Val Ser Arg Lys Pro Ser Leu Leu Thr Leu Gln Gly Pro Val Leu Ala 205 210 215 220			780
CCT GGG CAG AGC CTG ACC CTC CAG TGT GGC TCT GAT GTC GGC TAC GAC Pro Gly Gln Ser Leu Thr Leu Gln Cys Gly Ser Asp Val Gly Tyr Asp 225 230 235			828
AGA TTT GTT CTG TAT AAG GAG GGG GAA CGT GAC TTC CTC CAG CGC CCT Arg Phe Val Leu Tyr Lys Glu Gly Glu Arg Asp Phe Leu Gln Arg Pro 240 245 250			876
GGC CAG CAG CCC CAG GCT GGG CTC TCC CAG GCC AAC TTC ACC CTG GGC Gly Gln Gln Pro Gln Ala Gly Leu Ser Gln Ala Asn Phe Thr Leu Gly 255 260 265			924
CCT GTG AGC CCC TCC AAT GGG GGC CAG TAC AGG TGC TAC GGT GCA CAC			972

Pro Val Ser Pro Ser Asn Gly Gly Gln Tyr Arg Cys Tyr Gly Ala His	
270	275 280
AAC CTC TCC TCC GAG TGG TCG GCC CCC AGC GAC CCC CTG AAC ATC CTG	1020
Asn Leu Ser Ser Glu Trp Ser Ala Pro Ser Asp Pro Leu Asn Ile Leu	
285	290 295 300
ATG GCA GGA CAG ATC TAT GAC ACC GTC TCC CTG TCA GCA CAG CCG GGC	1068
Met Ala Gly Gln Ile Tyr Asp Thr Val Ser Leu Ser Ala Gln Pro Gly	
	305 310 315
CCC ACA GTG GCC TCA GGA GAG AAC GTG ACC CTG CTG TGT CAG TCA TGG	1116
Pro Thr Val Ala Ser Gly Glu Asn Val Thr Leu Leu Cys Gln Ser Trp	
	320 325 330
TGG CAG TTT GAC ACT TTC CTT CTG ACC AAA GAA GGG GCA GCC CAT CCC	1164
Trp Gln Phe Asp Thr Phe Leu Leu Thr Lys Glu Gly Ala Ala His Pro	
	335 340 345
CCA CTG CGT CTG AGA TCA ATG TAC GGA GCT CAT AAG TAC CAG GCT GAA	1212
Pro Leu Arg Leu Arg Ser Met Tyr Gly Ala His Lys Tyr Gln Ala Glu	
	350 355 360
TTC CCC ATG AGT CCT GTG ACC TCA GCC CAC GCG GGG ACC TAC AGG TGC	1260
Phe Pro Met Ser Pro Val Thr Ser Ala His Ala Gly Thr Tyr Arg Cys	
365	370 375 380
TAC GGC TCA CGC AGC TCC AAC CCC TAC CTG CTG TCT CAC CCC AGT GAG	1308
Tyr Gly Ser Arg Ser Ser Asn Pro Tyr Leu Leu Ser His Pro Ser Glu	
	385 390 395
CCC CTG GAG CTC GTG GTC TCA GGA CAC TCT GGA GGC TCC AGC CTC CCA	1356
Pro Leu Glu Leu Val Val Ser Gly His Ser Gly Gly Ser Ser Leu Pro	
	400 405 410
CCC ACA GGG CCG CCC TCC ACA CCT GGT CTG GGA AGA TAC CTG GAG GTT	1404
Pro Thr Gly Pro Pro Ser Thr Pro Gly Leu Gly Arg Tyr Leu Glu Val	
	415 420 425
TTG ATT GGG GTC TCG GTG GCC TTC GTC CTG CTG CTC TTC CTC CTC CTC	1452
Leu Ile Gly Val Ser Val Ala Phe Val Leu Leu Leu Phe Leu Leu Leu	
	430 435 440
TTC CTC CTC CTC CGA CGT CAG CGT CAC AGC AAA CAC AGG ACA TCT GAC	1500
Phe Leu Leu Leu Arg Arg Gln Arg His Ser Lys His Arg Thr Ser Asp	
445	450 455 460
CAG AGA AAG ACT GAT TTC CAG CGT CCT GCA GGG GCT GCG GAG ACA GAG	1548
Gln Arg Lys Thr Asp Phe Gln Arg Pro Ala Gly Ala Ala Glu Thr Glu	
	465 470 475
CCC AAG GAC AGG GGC CTG CTG AGG AGG TCC AGC CCA GCT GCT GAC GTC	1596
Pro Lys Asp Arg Gly Leu Leu Arg Arg Ser Ser Pro Ala Ala Asp Val	
	480 485 490
CAG GAA GAA AAC CTC TAT GCT GCC GTG AAG GAC ACA CAG TCT GAG GAC	1644
Gln Glu Glu Asn Leu Tyr Ala Ala Val Lys Asp Thr Gln Ser Glu Asp	
	495 500 505
GGG GTG GAG CTG GAC AGT CAG AGC CCA CAC GAT GAA GAC CCC CAC GCA	1692
Gly Val Glu Leu Asp Ser Gln Ser Pro His Asp Glu Asp Pro His Ala	
	510 515 520

GTG ACG TAT GCC CCG GTG AAA CAC TCC AGT CCT AGG AGA GAA ATG GCC 1740
 Val Thr Tyr Ala Pro Val Lys His Ser Ser Pro Arg Arg Glu Met Ala
 525 530 535 540

TCT CCT CCT TCC CCA CTG TCT GGG GAA TTC CTG GAC ACA AAG GAC AGA 1788
 Ser Pro Pro Ser Pro Leu Ser Gly Glu Phe Leu Asp Thr Lys Asp Arg
 545 550 555

CAG GCA GAA GAG GAC AGA CAG ATG GAC ACT GAG GCT GCT GCA TCT GAA 1836
 Gln Ala Glu Glu Asp Arg Gln Met Asp Thr Glu Ala Ala Ser Glu
 560 565 570

GCC TCC CAG GAT GTG ACC TAC GCC CAG CTG CAC AGC TTG ACC CTT AGA 1884
 Ala Ser Gln Asp Val Thr Tyr Ala Gln Leu His Ser Leu Thr Leu Arg
 575 580 585

CGG AAG GCA ACT GAG CCT CCT CCA TCC CAG GAG TTC GAG TCA GTC AGA 1932
 Arg Lys Ala Thr Glu Pro Pro Ser Gln Glu Phe Glu Ser Val Arg
 590 595 600

TCA GCA TTG T GAGGCCCAT CTCTACAAAA AATAAACCA GTCCGGCGTG GTGGCACAA 1991
 Ser Ala Leu
 605

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 623 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Thr Pro Ala Leu Thr Ala Leu Leu Cys Leu Gly Leu Ser Leu Gly
 -16 -15 -10 -5

Pro Arg Thr Arg Val Gln Ala Gly Pro Phe Pro Lys Pro Thr Leu Trp
 1 5 10 15

Ala Glu Pro Gly Ser Val Ile Ser Trp Gly Ser Pro Val Thr Ile Trp
 20 25 30

Cys Gln Gly Ser Leu Glu Ala Gln Glu Tyr Gln Leu Asp Lys Glu Gly
 35 40 45

Ser Pro Glu Pro Leu Asp Arg Asn Asn Pro Leu Glu Pro Lys Asn Lys
 50 55 60

Ala Arg Phe Ser Ile Pro Ser Met Thr Gln His His Ala Gly Arg Tyr
 65 70 75 80

Arg Cys His Tyr Tyr Ser Ser Ala Gly Trp Ser Glu Pro Ser Asp Pro
 85 90 95

Leu Glu Leu Val Met Thr Gly Ala Tyr Ser Lys Pro Thr Leu Ser Ala
 100 105 110

Leu Pro Ser Pro Val Val Ala Ser Gly Gly Asn Met Thr Leu Arg Cys
 115 120 125

Gly Ser Gln Lys Arg Tyr His His Phe Val Leu Met Lys Glu Gly Glu
 130 135 140
 His Gln Leu Pro Arg Thr Leu Asp Ser Gln Gln Leu His Ser Gly Gly
 145 150 155 160
 Phe Gln Ala Leu Phe Pro Val Gly Pro Val Asn Pro Ser His Arg Trp
 165 170 175
 Arg Phe Thr Cys Tyr Tyr Tyr Tyr Met Asn Thr Pro Arg Val Trp Ser
 180 185 190
 His Pro Ser Asp Pro Leu Glu Ile Leu Pro Ser Gly Val Ser Arg Lys
 195 200 205
 Pro Ser Leu Leu Thr Leu Gln Gly Pro Val Leu Ala Pro Gly Gln Ser
 210 215 220
 Leu Thr Leu Gln Cys Gly Ser Asp Val Gly Tyr Asp Arg Phe Val Leu
 225 230 235 240
 Tyr Lys Glu Gly Glu Arg Asp Phe Leu Gln Arg Pro Gly Gln Gln Pro
 245 250 255
 Gln Ala Gly Leu Ser Gln Ala Asn Phe Thr Leu Gly Pro Val Ser Pro
 260 265 270
 Ser Asn Gly Gly Gln Tyr Arg Cys Tyr Gly Ala His Asn Leu Ser Ser
 275 280 285
 Glu Trp Ser Ala Pro Ser Asp Pro Leu Asn Ile Leu Met Ala Gly Gln
 290 295 300
 Ile Tyr Asp Thr Val Ser Leu Ser Ala Gln Pro Gly Pro Thr Val Ala
 305 310 315 320
 Ser Gly Glu Asn Val Thr Leu Leu Cys Gln Ser Trp Trp Gln Phe Asp
 325 330 335
 Thr Phe Leu Leu Thr Lys Glu Gly Ala Ala His Pro Pro Leu Arg Leu
 340 345 350
 Arg Ser Met Tyr Gly Ala His Lys Tyr Gln Ala Glu Phe Pro Met Ser
 355 360 365
 Pro Val Thr Ser Ala His Ala Gly Thr Tyr Arg Cys Tyr Gly Ser Arg
 370 375 380
 Ser Ser Asn Pro Tyr Leu Leu Ser His Pro Ser Glu Pro Leu Glu Leu
 385 390 395 400
 Val Val Ser Gly His Ser Gly Gly Ser Ser Leu Pro Pro Thr Gly Pro
 405 410 415
 Pro Ser Thr Pro Gly Leu Gly Arg Tyr Leu Glu Val Leu Ile Gly Val
 420 425 430
 Ser Val Ala Phe Val Leu Leu Leu Phe Leu Leu Leu Phe Leu Leu Leu
 435 440 445
 Arg Arg Gln Arg His Ser Lys His Arg Thr Ser Asp Gln Arg Lys Thr
 450 455 460

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Asp Phe Gln Arg Pro Ala Gly Ala Ala Glu Thr Glu Pro Lys Asp Arg
465                      470                      475                      480

Gly Leu Leu Arg Arg Ser Ser Pro Ala Ala Asp Val Gln Glu Glu Asn
                      485                      490                      495

Leu Tyr Ala Ala Val Lys Asp Thr Gln Ser Glu Asp Gly Val Glu Leu
                      500                      505                      510

Asp Ser Gln Ser Pro His Asp Glu Asp Pro His Ala Val Thr Tyr Ala
                      515                      520                      525

Pro Val Lys His Ser Ser Pro Arg Arg Glu Met Ala Ser Pro Pro Ser
                      530                      535                      540

Pro Leu Ser Gly Glu Phe Leu Asp Thr Lys Asp Arg Gln Ala Glu Glu
545                      550                      555                      560

Asp Arg Gln Met Asp Thr Glu Ala Ala Ala Ser Glu Ala Ser Gln Asp
                      565                      570                      575

Val Thr Tyr Ala Gln Leu His Ser Leu Thr Leu Arg Arg Lys Ala Thr
                      580                      585                      590

Glu Pro Pro Pro Ser Gln Glu Phe Glu Ser Val Arg Ser Ala Leu
                      595                      600                      605

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(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1550 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 22..1438

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 22..67

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 70..1438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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GGAATTCGG GAGGAGACGC C ATG ATC CCC ACC TTC ACG GCT CTG CTC TGC      51
      Met Ile Pro Thr Phe Thr Ala Leu Leu Cys
      -16 -15                      -10

CTC GGG CTG AGT CTG GGC CCC AGT ACC CAC ATG CAG GCA GGG CCC CTC      99
Leu Gly Leu Ser Leu Gly Pro Ser Thr His Met Gln Ala Gly Pro Leu
      -5                      1                      5                      10

CCC AAA CCC ACC CTC TGG GCT GAG CCA GGC TCT GTG ATC AGC TGG GGG      147
Pro Lys Pro Thr Leu Trp Ala Glu Pro Gly Ser Val Ile Ser Trp Gly

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15	20	25	
AAC TCT GTG ACC ATC TGG TGT CAG GGG ACC CTG GAG GCT CGG GAG TAC Asn Ser Val Thr Ile Trp Cys Gln Gly Thr Leu Glu Ala Arg Glu Tyr 30 35 40			195
CGT CTG GAT AAA GAG GAA AGC CCA GCA CCC TGG GAC AGA CAG AAC CCA Arg Leu Asp Lys Glu Glu Ser Pro Ala Pro Trp Asp Arg Gln Asn Pro 45 50 55			243
CTG GAG CCC AAG AAC AAG GCC AGA TTC TCC ATC CCA TCC ATG ACA GAG Leu Glu Pro Lys Asn Lys Ala Arg Phe Ser Ile Pro Ser Met Thr Glu 60 65 70			291
GAC TAT GCA GGG AGA TAC CGC TGT TAC TAT CGC AGC CCT GTA GGC TGG Asp Tyr Ala Gly Arg Tyr Arg Cys Tyr Tyr Arg Ser Pro Val Gly Trp 75 80 85 90			339
TCA CAG CCC AGT GAC CCC CTG GAG CTG GTG ATG ACA GGA GCC TAC AGT Ser Gln Pro Ser Asp Pro Leu Glu Leu Val Met Thr Gly Ala Tyr Ser 95 100 105			387
AAA CCC ACC CTT TCA GCC CTG CCG AGT CCT CTT GTG ACC TCA GGA AAG Lys Pro Thr Leu Ser Ala Leu Pro Ser Pro Leu Val Thr Ser Gly Lys 110 115 120			435
AGC GTG ACC CTG CTG TGT CAG TCA CGG AGC CCA ATG GAC ACT TTT CTT Ser Val Thr Leu Leu Cys Gln Ser Arg Ser Pro Met Asp Thr Phe Leu 125 130 135			483
CTG ATC AAG GAG CGG GCA GCC CAT CCC CTA CTG CAT CTG AGA TCA GAG Leu Ile Lys Glu Arg Ala Ala His Pro Leu Leu His Leu Arg Ser Glu 140 145 150			531
CAC GGA GCT CAG CAG CAC CAG GCT GAA TTC CCC ATG AGT CCT GTG ACC His Gly Ala Gln Gln His Gln Ala Glu Phe Pro Met Ser Pro Val Thr 155 160 165 170			579
TCA GTG CAC GGG GGG ACC TAC AGG TGC TTC AGC TCA CAC GGC TTC TCC Ser Val His Gly Gly Thr Tyr Arg Cys Phe Ser Ser His Gly Phe Ser 175 180 185			627
CAC TAC CTG CTG TCA CAC CCC AGT GAC CCC CTG GAG CTC ATA GTC TCA His Tyr Leu Leu Ser His Pro Ser Asp Pro Leu Glu Leu Ile Val Ser 190 195 200			675
GGA TCC TTG GAG GGT CCC AGG CCC TCA CCC ACA AGG TCC GTC TCA ACA Gly Ser Leu Glu Gly Pro Arg Pro Ser Pro Thr Arg Ser Val Ser Thr 205 210 215			723
GCT GCA GGC CCT GAG GAC CAG CCC CTC ATG CCT ACA GGG TCA GTC CCC Ala Ala Gly Pro Glu Asp Gln Pro Leu Met Pro Thr Gly Ser Val Pro 220 225 230			771
CAC AGT GGT CTG AGA AGG CAC TGG GAG GTA CTG ATC GGG GTC TTG GTG His Ser Gly Leu Arg His Trp Glu Val Leu Ile Gly Val Leu Val 235 240 245 250			819
GTC TCC ATC CTG CTT CTC TCC CTC CTC CTC TTC CTC CTC CAA CAC Val Ser Ile Leu Leu Leu Ser Leu Leu Leu Phe Leu Leu Leu Gln His 255 260 265			867
TGG CGT CAG GGA AAA CAC AGG ACA TTG GCC CAG AGA CAG GCT GAT TTC			915

Trp Arg Gln Gly Lys His Arg Thr Leu Ala Gln Arg Gln Ala Asp Phe	
270 275 280	
CAA CGT CCT CCA GGG GCT GCC GAG CCA GAG CCC AAG GAC GGG GGC CTA	963
Gln Arg Pro Pro Gly Ala Ala Glu Pro Glu Pro Lys Asp Gly Gly Leu	
285 290 295	
CAG AGG AGG TCC AGC CCA GCT GCT GAC GTC CAG GGA GAA AAC TTC TGT	1011
Gln Arg Arg Ser Ser Pro Ala Ala Asp Val Gln Gly Glu Asn Phe Cys	
300 305 310	
GCT GCC GTG AAG GAC ACA CAG CCT GAG GAC GGG GTG GAA ATG GAC ACT	1059
Ala Ala Val Lys Asp Thr Gln Pro Glu Asp Gly Val Glu Met Asp Thr	
315 320 325 330	
CGG CAG AGC CCA CAC GAT GAA GAC CCC CAG GCA GTG ACG TAT GCC AAG	1107
Arg Gln Ser Pro His Asp Glu Asp Pro Gln Ala Val Thr Tyr Ala Lys	
335 340 345	
GTG AAA CAC TCC AGA CCT AGG AGA GAA ATG GCC TCT CCT CCC TCC CCA	1155
Val Lys His Ser Arg Pro Arg Arg Glu Met Ala Ser Pro Pro Ser Pro	
350 355 360	
CTG TCT GGG GAA TTC CTG GAC ACA AAG GAC AGA CAG GCA GAA GAG GAC	1203
Leu Ser Gly Glu Phe Leu Asp Thr Lys Asp Arg Gln Ala Glu Glu Asp	
365 370 375	
AGA CAG ATG GAC ACT GAG GCT GCT GCA TCT GAA GCC CCC CAG GAT GTG	1251
Arg Gln Met Asp Thr Glu Ala Ala Ala Ser Glu Ala Pro Gln Asp Val	
380 385 390	
ACT ACG CCC GGC TGC ACA GCT TTA CCC TCA GAC AGA AGG CAA CTG AGC	1299
Thr Thr Pro Gly Cys Thr Ala Leu Pro Ser Asp Arg Arg Gln Leu Ser	
395 400 405 410	
CTC CTC CAT CCC AGG AAG GGG CCT CTC CAG CTG AGC CCA GTG TCT ATG	1347
Leu Leu His Pro Arg Lys Gly Pro Leu Gln Leu Ser Pro Val Ser Met	
415 420 425	
CCA CTC TGG CCA TCC ACT AAT CCA GGG GGG ACC CAG ACC CCA CAA GCC	1395
Pro Leu Trp Pro Ser Thr Asn Pro Gly Gly Thr Gln Thr Pro Gln Ala	
430 435 440	
ATG GAG ACT CAG GAC CCC AGA AGG CAT GGA AGC TGC CTC CAG T	1438
Met Glu Thr Gln Asp Pro Arg Arg His Gly Ser Cys Leu Gln	
445 450 455	
AGACATCACT GAACCCACAGC CAGCCACAGAC CCCTGACACA GACCACTAGA AGATTCCGGG	1498
AACGTTGGGA GTCACCTGAT TCTGCAAAGA TAAATAATAT CCCTGCATTA TC	1550

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ile Pro Thr Phe Thr Ala Leu Leu Cys Leu Gly Leu Ser Leu Gly
 -16 -15 -10 -5
 Pro Ser Thr His Met Gln Ala Gly Pro Leu Pro Lys Pro Thr Leu Trp
 1 5 10 15
 Ala Glu Pro Gly Ser Val Ile Ser Trp Gly Asn Ser Val Thr Ile Trp
 20 25 30
 Cys Gln Gly Thr Leu Glu Ala Arg Glu Tyr Arg Leu Asp Lys Glu Glu
 35 40 45
 Ser Pro Ala Pro Trp Asp Arg Gln Asn Pro Leu Glu Pro Lys Asn Lys
 50 55 60
 Ala Arg Phe Ser Ile Pro Ser Met Thr Glu Asp Tyr Ala Gly Arg Tyr
 65 70 75 80
 Arg Cys Tyr Tyr Arg Ser Pro Val Gly Trp Ser Gln Pro Ser Asp Pro
 85 90 95
 Leu Glu Leu Val Met Thr Gly Ala Tyr Ser Lys Pro Thr Leu Ser Ala
 100 105 110
 Leu Pro Ser Pro Leu Val Thr Ser Gly Lys Ser Val Thr Leu Leu Cys
 115 120 125
 Gln Ser Arg Ser Pro Met Asp Thr Phe Leu Leu Ile Lys Glu Arg Ala
 130 135 140
 Ala His Pro Leu Leu His Leu Arg Ser Glu His Gly Ala Gln Gln His
 145 150 155 160
 Gln Ala Glu Phe Pro Met Ser Pro Val Thr Ser Val His Gly Gly Thr
 165 170 175
 Tyr Arg Cys Phe Ser Ser His Gly Phe Ser His Tyr Leu Leu Ser His
 180 185 190
 Pro Ser Asp Pro Leu Glu Leu Ile Val Ser Gly Ser Leu Glu Gly Pro
 195 200 205
 Arg Pro Ser Pro Thr Arg Ser Val Ser Thr Ala Ala Gly Pro Glu Asp
 210 215 220
 Gln Pro Leu Met Pro Thr Gly Ser Val Pro His Ser Gly Leu Arg Arg
 225 230 235 240
 His Trp Glu Val Leu Ile Gly Val Leu Val Val Ser Ile Leu Leu Leu
 245 250 255
 Ser Leu Leu Leu Phe Leu Leu Leu Gln His Trp Arg Gln Gly Lys His
 260 265 270
 Arg Thr Leu Ala Gln Arg Gln Ala Asp Phe Gln Arg Pro Pro Gly Ala
 275 280 285
 Ala Glu Pro Glu Pro Lys Asp Gly Gly Leu Gln Arg Arg Ser Ser Pro
 290 295 300
 Ala Ala Asp Val Gln Gly Glu Asn Phe Cys Ala Ala Val Lys Asp Thr
 305 310 315 320

Gln Pro Glu Asp Gly Val Glu Met Asp Thr Arg Gln Ser Pro His Asp
 325 330 335
 Glu Asp Pro Gln Ala Val Thr Tyr Ala Lys Val Lys His Ser Arg Pro
 340 345 350
 Arg Arg Glu Met Ala Ser Pro Pro Ser Pro Leu Ser Gly Glu Phe Leu
 355 360 365
 Asp Thr Lys Asp Arg Gln Ala Glu Glu Asp Arg Gln Met Asp Thr Glu
 370 375 380
 Ala Ala Ala Ser Glu Ala Pro Gln Asp Val Thr Thr Pro Gly Cys Thr
 385 390 395 400
 Ala Leu Pro Ser Asp Arg Arg Gln Leu Ser Leu Leu His Pro Arg Lys
 405 410 415
 Gly Pro Leu Gln Leu Ser Pro Val Ser Met Pro Leu Trp Pro Ser Thr
 420 425 430
 Asn Pro Gly Gly Thr Gln Thr Pro Gln Ala Met Glu Thr Gln Asp Pro
 435 440 445
 Arg Arg His Gly Ser Cys Leu Gln
 450 455

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1657 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 46..1588

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 94..1588

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 46..91

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCAGGAATTC GGCACGAGCA GAGCAGGGCA GTGGGAGGAG ACGCC ATG ACC CCC	54
Met Thr Pro	
-16 -15	
ATC CTC ACG GTC CTG ATC TGT CTC GGG CTG AGT CTG GGC CCC AGG ACC	102
Ile Leu Thr Val Leu Ile Cys Leu Gly Leu Ser Leu Gly Pro Arg Thr	
-10 -5 1	
CAC GTG CAG GCA GGG CAC CTC CCC AAG CCC ACC CTC TGG GCT GAG CCA	150
His Val Gln Ala Gly His Leu Pro Lys Pro Thr Leu Trp Ala Glu Pro	

5	10	15	
GGC TCT GTG ATC ATC CAG GGA AGT CCT GTG ACC CTC AGG TGT CAG GGG Gly Ser Val Ile Ile Gln Gly Ser Pro Val Thr Leu Arg Cys Gln Gly 20 25 30 35			198
AGC CTT CAG GCT GAG GAG TAC CAT CTA TAT AGG GAA AAC AAA TCA GCA Ser Leu Gln Ala Glu Glu Tyr His Leu Tyr Arg Glu Asn Lys Ser Ala 40 45 50			246
TCC TGG GTT AGA CGG ATA CAA GAG CCT GGG AAG AAT GGC CAG TTC CCC Ser Trp Val Arg Arg Ile Gln Glu Pro Gly Lys Asn Gly Gln Phe Pro 55 60 65			294
ATC CCA TCC ATC ACC TGG GAA CAC GCA GGG CGG TAT CAC TGT CAG TAC Ile Pro Ser Ile Thr Trp Glu His Ala Gly Arg Tyr His Cys Gln Tyr 70 75 80			342
TAC AGC CAC AAT CAC TCA TCA GAG TAC AGT GAC CCC CTG GAG CTG GTG Tyr Ser His Asn His Ser Ser Glu Tyr Ser Asp Pro Leu Glu Leu Val 85 90 95			390
GTG ACA GGA GCC TAC AGC AAA CCC ACC CTC TCA GCT CTG CCC AGC CCT Val Thr Gly Ala Tyr Ser Lys Pro Thr Leu Ser Ala Leu Pro Ser Pro 100 105 110 115			438
GTG GTG ACC TTA GGA GGG AAC GTG ACC CTC CAG TGT GTC TCA CAG GTG Val Val Thr Leu Gly Gly Asn Val Thr Leu Gln Cys Val Ser Gln Val 120 125 130			486
GCA TTT GAC GGC TTC ATT CTG TGT AAG GAA GGA GAA GAT GAA CAC CCA Ala Phe Asp Gly Phe Ile Leu Cys Lys Glu Gly Glu Asp Glu His Pro 135 140 145			534
CAA CGC CTG AAC TCC CAT TCC CAT GCC CGT GGG TGG TCC TGG GCC ATC Gln Arg Leu Asn Ser His Ser His Ala Arg Gly Trp Ser Trp Ala Ile 150 155 160			582
TTC TCC GTG GGC CCC GTG AGC CCG AGT CGC AGG TGG TCG TAC AGG TGC Phe Ser Val Gly Pro Val Ser Pro Ser Arg Arg Trp Ser Tyr Arg Cys 165 170 175			630
TAT GCT TAT GAC TCG AAC TCT CCC TAT GTG TGG TCT CTA CCC AGT GAT Tyr Ala Tyr Asp Ser Asn Ser Pro Tyr Val Trp Ser Leu Pro Ser Asp 180 185 190 195			678
CTC CTG GAG CTC CTG GTC CCA GGT GTT TCT AAG AAG CCA TCA CTC TCA Leu Leu Glu Leu Leu Val Pro Gly Val Ser Lys Lys Pro Ser Leu Ser 200 205 210			726
GTG CAG CCA GGT CCT ATG GTG GCC CCT GGG GAG AGC CTG ACC CTC CAG Val Gln Pro Gly Pro Met Val Ala Pro Gly Glu Ser Leu Thr Leu Gln 215 220 225			774
TGT GTC TCT GAT GTC GGC TAC GAC AGA TTT GTT CTG TAT AAG GAG GGA Cys Val Ser Asp Val Gly Tyr Asp Arg Phe Val Leu Tyr Lys Glu Gly 230 235 240			822
GAA CGT GAC TTC CTC CAG CGC CCT GGT TGG CAG CCC CAG GCT GGG CTC Glu Arg Asp Phe Leu Gln Arg Pro Gly Trp Gln Pro Gln Ala Gly Leu 245 250 255			870
TCC CAG GCC AAC TTC ACC CTG GGC CCT GTG AGC CCC TCC CAC GGG GGC			918

Ser	Gln	Ala	Asn	Phe	Thr	Leu	Gly	Pro	Val	Ser	Pro	Ser	His	Gly	Gly	
260							265				270					275
CAG	TAC	AGA	TGC	TAC	AGT	GCA	CAC	AAC	CTC	TCC	TCC	GAG	TGG	TCG	GCC	966
Gln	Tyr	Arg	Cys	Tyr	Ser	Ala	His	Asn	Leu	Ser	Ser	Glu	Trp	Ser	Ala	
				280					285					290		
CCC	AGT	GAC	CCC	CTG	GAC	ATC	CTG	ATC	ACA	GGA	CAG	TTC	TAT	GAC	AGA	1014
Pro	Ser	Asp	Pro	Leu	Asp	Ile	Leu	Ile	Thr	Gly	Gln	Phe	Tyr	Asp	Arg	
			295					300					305			
CCC	TCT	CTC	TCG	GTG	CAG	CCG	GTC	CCC	ACA	GTA	GCC	CCA	GGA	AAG	AAC	1062
Pro	Ser	Leu	Ser	Val	Gln	Pro	Val	Pro	Thr	Val	Ala	Pro	Gly	Lys	Asn	
			310				315					320				
GTG	ACC	CTG	CTG	TGT	CAG	TCA	CGG	GGG	CAG	TTC	CAC	ACT	TTC	CTT	CTG	1110
Val	Thr	Leu	Leu	Cys	Gln	Ser	Arg	Gly	Gln	Phe	His	Thr	Phe	Leu	Leu	
			325			330					335					
ACC	AAG	GAG	GGG	GCA	GGC	CAT	CCC	CCA	CTG	CAT	CTG	AGA	TCA	GAG	CAC	1158
Thr	Lys	Glu	Gly	Ala	Gly	His	Pro	Pro	Leu	His	Leu	Arg	Ser	Glu	His	
					345					350					355	
CAA	GCT	CAG	CAG	AAC	CAG	GCT	GAA	TTC	CGC	ATG	GGT	CCT	GTG	ACC	TCA	1206
Gln	Ala	Gln	Gln	Asn	Gln	Ala	Glu	Phe	Arg	Met	Gly	Pro	Val	Thr	Ser	
				360					365					370		
GCC	CAC	GTG	GGG	ACC	TAC	AGA	TGC	TAC	AGC	TCA	CTC	AGC	TCC	AAC	CCC	1254
Ala	His	Val	Gly	Thr	Tyr	Arg	Cys	Tyr	Ser	Ser	Leu	Ser	Ser	Asn	Pro	
			375					380					385			
TAC	CTG	CTG	TCT	CTC	CCC	AGT	GAC	CCC	CTG	GAG	CTC	GTG	GTC	TCA	GCA	1302
Tyr	Leu	Leu	Ser	Leu	Pro	Ser	Asp	Pro	Leu	Glu	Leu	Val	Val	Ser	Ala	
			390				395					400				
TCC	CTA	GGC	CAA	CAC	CCC	CAG	GAT	TAC	ACA	GTG	GAG	AAT	CTC	ATC	CGC	1350
Ser	Leu	Gly	Gln	His	Pro	Gln	Asp	Tyr	Thr	Val	Glu	Asn	Leu	Ile	Arg	
			405			410					415					
ATG	GGT	GTG	GCT	GGC	TTG	GTC	CTG	GTG	GTC	CTC	GGG	ATT	CTG	CTA	TTT	1398
Met	Gly	Val	Ala	Gly	Leu	Val	Leu	Val	Val	Leu	Gly	Ile	Leu	Leu	Phe	
					425					430					435	
GAG	GCT	CAG	CAC	AGC	CAG	AGA	AGC	CTA	CAA	GAT	GCA	GCC	GGG	AGT	GAA	1446
Glu	Ala	Gln	His	Ser	Gln	Arg	Ser	Leu	Gln	Asp	Ala	Ala	Gly	Ser	Glu	
				440					445					450		
CAG	CAG	AGA	GGA	CAA	TGC	ATC	CTT	CAG	CGT	GGT	GGA	GCC	TCA	GGG	ACA	1494
Gln	Gln	Arg	Gly	Gln	Cys	Ile	Leu	Gln	Arg	Gly	Gly	Ala	Ser	Gly	Thr	
			455					460					465			
GAT	CTG	ATG	ATC	CCA	GGA	GGC	TCT	GGA	GGA	CAA	TCT	AGG	ACC	TAC	ATT	1542
Asp	Le															

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 514 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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Met Thr Pro Ile Leu Thr Val Leu Ile Cys Leu Gly Leu Ser Leu Gly
-16 -15                      -10                      -5

Pro Arg Thr His Val Gln Ala Gly His Leu Pro Lys Pro Thr Leu Trp
 1              5              10              15

Ala Glu Pro Gly Ser Val Ile Ile Gln Gly Ser Pro Val Thr Leu Arg
      20      25      30

Cys Gln Gly Ser Leu Gln Ala Glu Glu Tyr His Leu Tyr Arg Glu Asn
      35      40      45

Lys Ser Ala Ser Trp Val Arg Arg Ile Gln Glu Pro Gly Lys Asn Gly
      50      55      60

Gln Phe Pro Ile Pro Ser Ile Thr Trp Glu His Ala Gly Arg Tyr His
      65      70      75      80

Cys Gln Tyr Tyr Ser His Asn His Ser Ser Glu Tyr Ser Asp Pro Leu
      85      90      95

Glu Leu Val Val Thr Gly Ala Tyr Ser Lys Pro Thr Leu Ser Ala Leu
      100      105      110

Pro Ser Pro Val Val Thr Leu Gly Gly Asn Val Thr Leu Gln Cys Val
      115      120      125

Ser Gln Val Ala Phe Asp Gly Phe Ile Leu Cys Lys Glu Gly Glu Asp
      130      135      140

Glu His Pro Gln Arg Leu Asn Ser His Ser His Ala Arg Gly Trp Ser
      145      150      155      160

Trp Ala Ile Phe Ser Val Gly Pro Val Ser Pro Ser Arg Arg Trp Ser
      165      170      175

Tyr Arg Cys Tyr Ala Tyr Asp Ser Asn Ser Pro Tyr Val Trp Ser Leu
      180      185      190

Pro Ser Asp Leu Leu Glu Leu Leu Val Pro Gly Val Ser Lys Lys Pro
      195      200      205

Ser Leu Ser Val Gln Pro Gly Pro Met Val Ala Pro Gly Glu Ser Leu
      210      215      220

Thr Leu Gln Cys Val Ser Asp Val Gly Tyr Asp Arg Phe Val Leu Tyr
      225      230      235      240

Lys Glu Gly Glu Arg Asp Phe Leu Gln Arg Pro Gly Trp Gln Pro Gln
      245      250      255

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Ala Gly Leu Ser Gln Ala Asn Phe Thr Leu Gly Pro Val Ser Pro Ser
 260 265 270
 His Gly Gly Gln Tyr Arg Cys Tyr Ser Ala His Asn Leu Ser Ser Glu
 275 280 285
 Trp Ser Ala Pro Ser Asp Pro Leu Asp Ile Leu Ile Thr Gly Gln Phe
 290 295 300
 Tyr Asp Arg Pro Ser Leu Ser Val Gln Pro Val Pro Thr Val Ala Pro
 305 310 315 320
 Gly Lys Asn Val Thr Leu Leu Cys Gln Ser Arg Gly Gln Phe His Thr
 325 330 335
 Phe Leu Leu Thr Lys Glu Gly Ala Gly His Pro Pro Leu His Leu Arg
 340 345 350
 Ser Glu His Gln Ala Gln Gln Asn Gln Ala Glu Phe Arg Met Gly Pro
 355 360 365
 Val Thr Ser Ala His Val Gly Thr Tyr Arg Cys Tyr Ser Ser Leu Ser
 370 375 380
 Ser Asn Pro Tyr Leu Leu Ser Leu Pro Ser Asp Pro Leu Glu Leu Val
 385 390 395 400
 Val Ser Ala Ser Leu Gly Gln His Pro Gln Asp Tyr Thr Val Glu Asn
 405 410 415
 Leu Ile Arg Met Gly Val Ala Gly Leu Val Leu Val Val Leu Gly Ile
 420 425 430
 Leu Leu Phe Glu Ala Gln His Ser Gln Arg Ser Leu Gln Asp Ala Ala
 435 440 445
 Gly Ser Glu Gln Gln Arg Gly Gln Cys Ile Leu Gln Arg Gly Gly Ala
 450 455 460
 Ser Gly Thr Asp Leu Met Ile Pro Gly Gly Ser Gly Gly Gln Ser Arg
 465 470 475 480
 Thr Tyr Ile Ile Trp Thr Val Cys Trp Ser Phe Leu Glu Thr Ala Ile
 485 490 495
 Asn Ile

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Ala	Pro	Thr	Leu	Pro	Ala	Leu	Leu	Cys	Leu	Gly	Leu	Ser	Val	Gly	1	5	10	15
Leu	Arg	Thr	Gln	Val	Gln	Ala	Gly	Thr	Phe	Pro	Lys	Pro	Ile	Ile	Trp	20	25	30	
Ala	Glu	Pro	Ser	Ser	Val	Val	Pro	Leu	Gly	Ser	Ser	Val	Thr	Ile	Leu	35	40	45	
Cys	Gln	Gly	Pro	Pro	Asn	Thr	Lys	Ser	Phe	Ser	Leu	Asn	Lys	Glu	Gly	50	55	60	
Asp	Ser	Thr	Pro	Trp	Asn	Ile	His	Pro	Ser	Leu	Glu	Pro	Trp	Asp	Lys	65	70	75	80
Ala	Asn	Phe	Phe	Ile	Ser	Asn	Val	Arg	Glu	Gln	Gln	Ala	Gly	Arg	Tyr	85	90	95	
His	Cys	Ser	His	Phe	Ile	Gly	Val	Asn	Trp	Ser	Glu	Pro	Ser	Glu	Pro	100	105	110	
Leu	Asp	Leu	Leu	Val	Ala	Gly	Glu	Glu	Pro	Ala	Gly	Arg	Leu	Arg	Asp	115	120	125	
Arg	Pro	Ser	Leu	Ser	Val	Arg	Pro	Ser	Pro	Ser	Val	Ala	Pro	Gly	Glu	130	135	140	
Asn	Val	Thr	Leu	Leu	Cys	Gln	Ser	Gly	Asn	Arg	Thr	Asp	Thr	Phe	Leu	145	150	155	160
Leu	Ser	Lys	Glu	Gly	Ala	Ala	His	Arg	Pro	Leu	Arg	Leu	Arg	Ser	Gln	165	170	175	
Asp	Gln	Asp	Gly	Trp	Tyr	Gln	Ala	Glu	Phe	Ser	Leu	Ser	Pro	Val	Thr	180	185	190	
Ser	Ala	His	Gly	Gly	Thr	Tyr	Arg	Cys	Tyr	Arg	Ser	Leu	Ser	Thr	Asn	195	200	205	
Pro	Tyr	Leu	Leu	Ser	Gln	Pro	Ser	Glu	Pro	Leu	Ala	Leu	Leu	Val	Ala	210	215	220	
Asp	Tyr	Thr	Met	Gln	Asn	Leu	Ile	Arg	Met	Gly	Leu	Ala	Ala	Ser	Val	225	230	235	240
Leu	Leu	Leu	Leu	Gly	Ile	Leu	Leu	Cys	Gln	Ala	Arg	His	Asp	His	Gly	245	250	255	
Gly	Ala	Arg	Glu	Ala	Ala	Arg	Ser	260											

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```

GGTCACGAGC CTNIGTCCTG GCCAGNCACC GAGGGNTCAT CCATCCACAG AGCAGTGCAG      60
TGGGAGGAGC CGNGATGACC CCCATCCTCA AGGTCCTGAT CTGTCTCGGG CCCCTCCCCA      120
AGCCNACCCT CTGGGCTGAG CCAGGCTCTG TGATCANCNA AGGGGAGTCC TGTANCCCTN      180
AGGTGT                                           186

```

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

GGCAGNAGGG NCCCCTCCCC AAGCCCACCC TCTGGGACTG AGCCAGGCTC TGTAAATCACC      60
CAAGGNAGTC CTGTAACCCT NAGGTGTNAG GGGAGCCTGG AGACGCAGGA GTACCATCTA      120
TATAGAGAAA AGAAAACAGC ACTCTGGATT ACACGGATCC CACAGGAGCT TGTAAAGAAG      180
GGCCAGTTC CCATCCTATC CATCACCTGG GAACATGCAG GCGGGTATTC TGTATCTTGG      240
NAGCCACATT NAAGNCCTNT AGGGGCAGTN                                           270

```

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs.
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```

GGTCCTNAAT CTGTNTCGAA GCCTACAGCA AACCCACCCT CTAAGCTCTG CCCAGCCCTG      60
TGGTGACCTT AGGAGGGAAC GTGAACCCTC CAGTGTGTCT AAAAGGTGEN ATTTGAANGG      120
CTTCATCTCTG TGTAAGGTAA GGAGAAGATG AACACCCACA ACGCCTGANC TCCCATTCNN      180
ATGCCCGTGG GTGGTCTCTG GCCATCTTCT CCGTGGGCCC CGTGAGCCCG AGTGGCAGTG      240
GGTCGTACAG GTGCTATGNT TGNTAATTNG GAANTGTGCC CTATGANNTG GGTGTTNTAA      300

```

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 253 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGCAGGAGCC TACAGGTGCT ACGGCTCACT CAGCTCCAAC CCCTACCTGC TGACTCACCC	60
CAGTNACCCC CTGGAGCTCG TGGTCTCAGG AGCAGCTGAG ACCCTCAGCC CACCACAAA	120
CAAGTCCGAC TCCAAGGCTG GTGAGTGAGG AGATGCTTGC CGTGATGACG CTGGGCACAG	180
AGGGTCAGGT CCTNCAAGA GGAGCTGGGT GTCCTNGGTG GACATTNAA GAATTATATT	240
NATTGCANCT TGA	253

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 197 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TAATTCGGCA GAGCGGGCGG GGACAATAAG GGAATAAAAG CTGGCGAGCN CGGCACCCCA	60
CCAGAGTCTG CTTCCACGTT GTGGNAGCTT TGTTCTCTTG CTCTACACAA TAAATCTTGC	120
TGCTGCTAAA AAAAAAAAAA AAAAAAAAAA AAAAAATTTN GGGGGTCCNA AAAAAAAAAAG	180
AAAGGGAAAG GNTTTTT	197

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 495 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AATTCGGCAG AGAGTNGTTC GGCCCCCAGC GACCCCTGA ACATCCTGAT GGCAGGACAG	60
--	----

ATCTATGACA CCGTCTCCCT GTCAGCACAG CCGGGCCCCA CAGTGGCCTC AGGAGAGAAC	120
GTGAACCCCTG NCTGTGTCAG TNCATGGTGG TCAGTTTGAC ACTTTCCTTC TGACCAAAGA	180
AGGGGCAGCC CATCCCCAC TGCCTCTGAG ATCAATGTAC GGAGCTCATA AGTACCAGGC	240
TGAAATTCCC CATGAGTCCT GTGAACCTCA GCCCAGCGG GGNACCTACA GGTGCTAACG	300
GNTCACGNAG TTCCAACCCC CACCTGNTGT NTTCACCCA GTNGGCNCCC TGGGAGCTCG	360
TTGGTTTTC GACAAATTTT GGGGGNTTNC ANNTTCNAN GCCAAAAGGN CNGTCTTTC	420
NAANTGGTTT TGGGNAGATA ACTTGGNGGT TTTNAATTGG GGTTTTGGTT GGGCTTTGGG	480
CNTGTGTTT TGCCT	495

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 397 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AATTCGGCAG AGNCAGCACT GAGGGCTCAT CCCTCTGCAG AGCGCGGGGT CACCGTAAG	60
GAGACGCCAT GACGCCCGCC CTCACAGCCC TGCTCTGCCT TGGGCTGAGT CTGGGCCCCA	120
GGAACCCGCG TGGCAGGCAG GGCCCTTCCC CAAACCCACC CTCTGGGGCT GAGCCAGGCT	180
CTGTGAATCA GCTGGGGGGA GCCCCGTGAA CCATCTGGTG TCAGGGGGAG CCTGGAGGNC	240
CAGGAGTACC AACTGGATAA AGAAGGGAAG CCCAGAGCCC TTGGGACAGA AATAACCCAC	300
TGGGAACCCA AGGAACAAGG GCCAGATTTT TGCATNNCCA TTNCATGGAT ACAGNAACCT	360
TGNNAGGGGA GGATTACCGG TTGNCAATT ATTAACA	397

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 445 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AATTCGGCAN AGCCACAAGG TCCGTNTCAA CAGCTGGCCC TGAGGACCAG CCCCTTATGC	60
---	----

CTACAGGGTC AGTCCCNAC AGTGGTCTGA GAAGGCACTG NGAGGTACTG ATCGGGGTCT	120
TGGTGGTCTN CATCCTGCTT CTTTCCCTCC TCCTCTTCCT CCTCCTCCAA CACTGGCGTC	180
AGGGAAAACA CAGGACATTG GCCCAGAGAC AGGCTGATTT CCAACGTCCT CCAGGGGCTG	240
CCGAGCCAGA GCCCAAGGAC GGGGGCCTAC AGAGGAGGTN CAGCCCAGTT CTTGACGTTT	300
CAGGGAGAAA AATTTTITGN TTNCGTNAAG GACAAAAAAG CTTNGGGACG GGGTTGGAAT	360
TGNC AATTGG GANNGCCCAN AAGTTTAAGA NCCCCNGNA TTTANGNTTT NCAAGTNTA	420
AAAATTTCAN ACTTTGGGGG GAATT	445

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AATTCGGCAC GAGGTACTGG GAGGTACTGA TCGGGGTCTT GGTGGTCTCC ANCCTGCTTC	60
TNTCCNTCCT CCTCTTCCTC CTCCTCCAAC ACTGGCGTCA GGGAAAACAC AGGACATTGG	120
CCCAGAGACA GGNTGATTTN CAACGTCCTC CAGGGGCTGC CGAGCCAGAG CCCAAGGACG	180
GGGGCCTACA GAGGAGGTCC AGCCCAGNTG CTGACGTNCA GGGAGAAAAC TTNTGTGCTN	240
CCGTGAAGAA CACACAGNCT	260

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CGGAAAGCCC AGCACCCTTG ANNAGANAGA ACCCACTGGA GCCCAAGAAC AAGGCCAGAT	60
TCTCGATCCC ATCCATGGAC AGAGGACTAT GCAGGGAGAT ACCGCTGTTA ACTATCGCAG	120
CCCTGTAGGC TGGGTGCACA CCNAGGTGAA CCCCTGNTG NCTGGGAGAT GGTGAGGAGC	180
CTAGAGTAAA CCCACCCTTT AAGGCCCTGC CGAGTCCTCT TGTANCCNCA GTGAAAGAGC	240
GTGACCCTGC TGTNT	255

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

AATTCCGGCC TCTCCTCCCT CCCCACTGTC TGGGGAATTC CTGGACACAA AGGACAGACA      60
GGCAGAAGAG GACAGACAGA TGGACACTGA GGCTGCTGCA TCTAAAGCCC CCCAGGATGT      120
GAACCTACGC CCAGCTGCAC AGTTTACCCT CAGACAGAAG GCAACTGAGC CTCCTCCATC      180
CCAGGAAGGG GCCTCTNCAG CTGAGCCCAG TGTCTATGCC ACTCTGGCCA TCCACTTAAT      240
CCAGGGGGGA CCCAGACCCC ACAAGCCATG GAGATTCAGG ACCNNAGAAG GCATGGAAGN      300
TGCCTTCCAG TAGACATCAN TGAACCCCAG NCAGNCCAGA ACCTTNANAA AGACCATTAG      360
AAGTTTNGG GGAAGTTTGG GGGTGAATTG NTTTTGGAA AGGTAAATA ATTNTNCTG      420
GNATTTTNA AATTAAAGTT GGGAGACTTT TTAATTNNA ATGGGGTTTA TTGNITNAAA      480
AAANNNGNN NGTNGNN                                     497

```

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```

AATTCGGCAC GACCTTTCCT CCTCCTCTCC CTCCTCCTCC TCCGTCAGCN TCACAGCAAA      60
CACAGGACAT CTGACCAGAG AAAGACTGAT TTCCAGCGTC CTGCAGGGGC TGCGGAGACA      120
GAGCCCAAGG ACAGGGGCCT GCTGAGGAGG TCCAGCCCAG CTGCTGACGT CCAGGAAGAA      180
AACCTCTGTA AGAGGAAGAG AGGGGACAAA TGGGGTGCT GGAGAGACAG GAGTCCCAAA      240
ATTTCACTAG CAACAGGGAG GGGCTGGGAA GGGTCTGGGG CTCCGTGGAA GATGGTCTTN      300
CCCCACTG TNGGACCTC CCTGCATTCG GTGGCCCTT TGGGAGCAGG GCAGGGGGCC      360
AGCAGGATTN AGAGGTTTTA GAGAACCAGG NGANGANCCC TTTGTTTTGN CCCAGNAGTT      420

```

GGTGTTTTIN AGGGACAAAA ATTTTNGGN NAGGTTGGAG TTTGNNNATT NAGAGCCCNA 480
 AGGTTNNGGN CCCCGGNAT TNGTTTTCC CC 512

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GGTCCTNAAT CTGTNTCGAA GCCTACAGCA AACCCACCCT CTAAGCTCTG CCCAGCCCTG 60
 TGGTGACCTT AGGAGGGAAC GTGAACCTC CAGTGTGTCT AAAAGGTGGN ATTGAANGG 120
 CTTTATCTG TGTAAAGTAA GGAGAAGATG AACACCCACA ACGCCTGANC TCCCATTCN 180
 ATGCCCGTGG GTGGTCCTGG GCCATCTTCT CCGTGGGCC CGTGAGCCCG AGTGGCAGTG 240
 GGTCGTACAG GTGCTATGNT TGNTAATTNG GAANTGTGCC CTATGANNTG GGTGTTNTAA 300

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GACTCATGAC TGAGCCAGGC TCTGTGATCA CCC 33

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GACAGATCTC TCACCAGCCT TGGAGTC 27

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GACAGATCTG AGCCAGGCTC TGTGATCACC C

31

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GACTCTAGAG TCCACCCAGG ACACCCAGC

29

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CTAGCCAGAT CTGCCACCAT GAACTCCTTC TCCACAAGCG CCTTCGGTCC AGTTGCCTTC

60

TCCCTGGGGC TGCTCCTGGT GTTGCTGCT GCCTTCCCTG CCCAGTTGT GAGAGAGCCA

120

GGCTCTGTGA TCACCC

136

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CAGCTCGAGC TCACCAGCCT TGGAGTC

27

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CTAGCCGGAT CCGCCACCAT GAACTCCTTC TCCACAAGCG CCTTCGGTCC AGTTGCCTTC
TCCCTGGGGC TGCTCCTGGT GTTGCTGCT GCCTTCCCTG CCCAGTTGT GAGAGAGCCA
GGCTCTGTGA TCACCC

60

120

136

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GCTCTAGAGT CCACCCAGGA CACCCAGC

28